



SEQUENCE LISTING

<110> ANDREW, DAVID P.
LEWIN, DAVID A.
PENNICA, DIANE
RASTELLI, LUCA
TALLION, BRUCE

<120> WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC
ACIDS ENCODING SAME

<130> 11669.191USC1

<140> 10/614,599

<141> 2003-07-07

<150> 09/715,747

<151> 2000-11-17

<150> 09/715,418

<151> 2000-11-16

<150> 60/166,177

<151> 1999-11-18

<160> 49

<170> PatentIn Ver. 2.1

<210> 1

<211> 212

<212> DNA

<213> Mus sp.

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<222> (1541)

<223> "n" represents a, t, c, g, other or unknown

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<210> 3
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      20              25              30

Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val Glu Arg Ala
      35              40              45

Ile Glu Thr Leu Ile Lys Asn Phe His Lys Tyr Ser Val Ala Gly Lys
      50              55              60

Lys Glu Thr Leu Thr Pro Ala Glu Leu Arg Asp Leu Val Thr Gln Gln
      65              70              75              80

Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala
      85              90              95

Asn Leu Gly Asn Cys Asn Asp Ser Lys Leu Glu Phe Gly Ser Phe Trp
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Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Met Glu Arg Pro Val
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Thr Arg Ser
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<210> 4
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<212> DNA
<213> Homo sapiens

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<223> "n" represents a, t, c, g, other or unknown

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<222> (337)
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agagaaaatt gccaacctgg gcagctgcaa tgactctaaa ctggagttca ggagtttctg 300
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<211> 379
<212> DNA
<213> Homo sapiens

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caggttgcca attttctctt ccaggccaca gttgctcggc atgagatggg gcagctgctg 180
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ctggtgaaag ttcttgatga ggggtctcaat ggccctctcc acatcactga attcctgagc 300
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gagagttctg ttgtcctat 379

<210> 6
<211> 118
<212> PRT
<213> Homo sapiens

<400> 6
Asp Asn Arg Thr Leu Thr Lys Gly Pro Asp Thr Val Ser Thr Met Gly
1 5 10 15
Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp Val
20 25 30

Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val
 35 40 45
 Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val
 50 55 60
 Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu
 65 70 75 80
 Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
 85 90 95
 Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Leu Glu
 100 105 110
 Arg Pro Val Arg Gly His
 115

<210> 7
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 7
 cttgatgagg gtctcaatgg 20

<210> 8
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Probe

<400> 8
 ccacatcact gaattcctga gcatcc 26

<210> 9
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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 cagacacagt gagcaccatg 20

<210> 10

<211> 98
 <212> PRT
 <213> Homo sapiens, W27152, chemotactic cytokine II CCII from WO97/34013

<400> 10
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 20 25 30
 Leu Ser Val Asn Glu Phe Lys Glu Leu Val Thr Gln Gln Leu Pro His
 35 40 45
 Leu Leu Lys Asp Val Gly Ser Leu Asp Glu Lys Met Lys Ser Leu Asp
 50 55 60
 Val Asn Gln Asp Ser Glu Leu Lys Phe Asn Glu Tyr Trp Arg Leu Ile
 65 70 75 80
 Gly Glu Leu Ala Lys Glu Ile Arg Lys Lys Lys Asp Leu Lys Ile Arg
 85 90 95
 Lys Lys

<210> 11
 <211> 110
 <212> PRT
 <213> Homo sapiens, G491246, Macrophage Migration Inhibition Factor (MRP-14)

<400> 11
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 Gln Tyr Ser Val Lys Leu Gly His Pro Asp Thr Leu Asn Gln Gly Glu
 20 25 30
 Phe Lys Glu Leu Val Arg Lys Asp Leu Gln Asn Phe Leu Lys Lys Glu
 35 40 45
 Asn Lys Asn Glu Lys Val Ile Glu His Ile Met Glu Asp Leu Asp Thr
 50 55 60
 Asn Ala Asp Lys Gln Leu Ser Phe Glu Glu Phe Ile Met Leu Met Ala
 65 70 75 80
 Arg Leu Thr Trp Ala Ser His Glu Lys Met His Glu Gly Asp Glu Gly
 85 90 95
 Pro Gly His His His Lys Pro Gly Leu Gly Glu Gly Thr Pro
 100 105 110

<210> 12

<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

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1 5 10 15
Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala
20 25 30
Ala Lys Ser Val Lys
35

<210> 13
<211> 37
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: 3-100/ICaBP type
calcium binding protein

<400> 13
Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
1 5 10 15
Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
20 25 30
Leu Val Thr Gln Gln
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<210> 14
<211> 19
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Bacterial type II
secretion system protein F

<400> 14
Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu
1 5 10 15
Glu Lys Ile

<210> 15
<211> 10
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Ubiquitin
carboxyl-terminal hydrolases family

<400> 15
Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
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<210> 16
<211> 49
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Bacterial
themataxis sensory transducers protein

<400> 16
Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr
1 5 10 15
Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
20 25 30
Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
35 40 45

Phe

<210> 17
<211> 32
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Phosphoenolpyruvate carboxykinase (ATP) protein

<400> 17
Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
1 5 10 15
Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

<210> 18
<211> 33

<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Prokaryotic-type
carbonic anhydrases proteins

<400> 18
His Gln Tyr Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
1 5 10 15
Leu Arg Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn
20 25 30

Cys

<210> 19
<211> 15
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Ergosterol
biosynthesis ERG4/ERG24 family protein

<400> 19
Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg
1 5 10 15

<210> 20
<211> 25
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Lysosome-associated membrane glycoproteins du

<400> 20
Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly
1 5 10 15

Ser Cys Asn Asp Ser Lys Ile Glu Phe
20 25

<210> 21
<211> 39
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:
Phosphofructokinase proteins

<400> 21
 Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys
 1 5 10 15
 Asn Asp Ser Lys Leu Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu
 20 25 30
 Ala Ala Lys Ser Val Lys Leu
 35

<210> 22
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 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: PH domain
 proteins profile

<400> 22
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 1 5 10

<210> 23
 <211> 45
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Myotoxins
 protein

<400> 23
 Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
 1 5 10 15
 Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu Phe Arg Ser
 20 25 30
 Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
 35 40 45

<210> 24
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 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism:
 Phosphatidylinositol-specific phospholipase X

<400> 24

Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile Ala Asn Leu Gly Ser
 1 5 10 15

Cys

<210> 25

<211> 45

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glypicans
 protein

<400> 25

Met Gly Gly Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
 1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
 20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu
 35 40 45

<210> 26

<211> 10

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Membrane attack
 complex components/perforin

<400> 26

Ile Lys Asn Phe His Gln Tyr Ser Val Glu
 1 5 10

<210> 27

<211> 44

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Urease nickel
 ligands protein

<400> 27

Thr Leu Ile Lys Asn Phe His Gln Tyr Ser Val Glu Gly Gly Lys Glu
 1 5 10 15

Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln Leu Pro
 20 25 30

His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys
 35 40

<210> 28
 <211> 13
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Phosphoglycerate
 mutase family phosphohistidi

<400> 28
 Gln Glu Phe Ser Asp Val Glu Arg Ala Ile Glu Thr Leu
 1 5 10

<210> 29
 <211> 10
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Ribosomal protein
 L23 protein

<400> 29
 Glu Leu Arg Asp Leu Val Thr Gln Gln Leu
 1 5 10

<210> 30
 <211> 41
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism:
 2'-5'-oligoadenylate synthetases protein

<400> 30
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 1 5 10 15

Glu Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val
 20 25 30

Lys Leu Glu Arg Pro Val Arg Gly His
 35 40

<210> 31
 <211> 24
 <212> PRT
 <213> Unknown Organism

<220>

<223> Description of Unknown Organism: Formate and
nitrite transporters protein

<400> 31

Asp Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly
1 5 10 15

Leu Glu Glu Lys Ile Ala Asn Leu
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<210> 32

<211> 34

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Glycoprotein
hormones beta chain protein

<400> 32

Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser Asp
1 5 10 15

Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
20 25 30

Val Glu

<210> 33

<211> 21

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Vinculin family
talin-binding region protein

<400> 33

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
1 5 10 15

Leu Pro His Leu Met
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<210> 34

<211> 40

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Beta-lactamases
clas B protein

<400> 34

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1 5 10 15

Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu Val Thr Gln Gln
20 25 30

Leu Pro His Leu Met Pro Ser Asn
35 40

<210> 35

<211> 21

<212> PRT

<213> Unknown Organism

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<223> Description of Unknown Organism: Heat shock hsp20
protein family profile

<400> 35

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1 5 10 15

Val Lys Leu Glu Arg
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<210> 36

<211> 35

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism:
Hydroxymethylglutaryl-coenzyme A lyase protein

<400> 36

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1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
20 25 30

Ser Val Glu
35

<210> 37

<211> 294

<212> DNA

<213> Mus sp.

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<210> 38
<211> 43
<212> PRT
<213> Homo sapiens

<400> 38
Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr Ser
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Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp Leu
20 25 30
Val Thr Gln Gln Leu Pro His Leu Met Pro Ser
35 40

<210> 39
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<212> PRT
<213> Homo sapiens translation of GenBank Accession AAY007220

<400> 39
Met Gly Gln Cys Arg Ser Ala Asn Ala Glu Asp Ala Gln Glu Phe Ser
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20 25 30
Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
35 40 45
Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu
50 55 60
Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu
65 70 75 80
Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
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Leu Glu Arg Pro Val Arg Gly His
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<210> 40
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<212> PRT

<220>

<223> Description of Artificial Sequence: Consensus sequence

<400> 40

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1 5 10 15

Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Tyr Ser
20 25 30

Val Gly Lys Glu Thr Leu Thr Pro Glu Leu Arg Asp Leu Val Thr Gln
35 40 45

Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu Glu Glu Lys Ile
50 55 60

Ala Asn Leu Gly Cys Asn Asp Ser Lys Leu Glu Phe Ser Phe Trp Glu
65 70 75 80

Leu Ile Gly Glu Ala Ala Lys Ser Val Lys Glu Arg Pro Val
85 90

<210> 41

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: gi/4139958/pdb/1MHO

<400> 41

Glu Lys Ala Val Val Ala Leu Ile Asp Val Phe His Gln Tyr Ser Gly
1 5 10 15

Arg Glu Gly Asp Lys His Lys Leu Lys Lys Ser Glu Leu Lys Glu Leu
20 25 30

Ile Asn Asn Glu Leu Ser His Phe Leu
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<210> 42

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Protein MRP-126

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Glu Lys Ala Ile Asp Val Ile Ile Asp Val Phe His Gln Tyr Ser Arg
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<210> 49

<211> 104

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Consensus
 sequence

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Asp Val Glu Arg Ala Ile Glu Thr Leu Ile Lys Asn Phe His Gln Tyr
 20 25 30

Ser Val Glu Gly Gly Lys Glu Thr Leu Thr Pro Ser Glu Leu Arg Asp
 35 40 45

Leu Val Thr Gln Gln Leu Pro His Leu Met Pro Ser Asn Cys Gly Leu
 50 55 60

Glu Glu Lys Ile Ala Asn Leu Gly Ser Cys Asn Asp Ser Lys Leu Glu
 65 70 75 80

Phe Arg Ser Phe Trp Glu Leu Ile Gly Glu Ala Ala Lys Ser Val Lys
 85 90 95

Leu Glu Arg Pro Val Arg Gly His
 100

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1

5

10

15

Arg Glu Gly Asp Lys Asp Thr Leu Thr Arg Lys Glu Leu Lys Leu Leu
 20 25 30

Ile Glu Lys Gln Leu Ala Asn Tyr Leu
 35 40

<210> 43

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: ICTACALCIN

<400> 43

Gln Lys Gly Met Ala Leu Leu Ile Ser Thr Phe His Lys Tyr Ser Gly
 1 5 10 15

Lys Glu Gly Asp Lys Cys Thr Leu Thr Lys Gly Glu Leu Lys Asp Leu
 20 25 30

Ile Thr Lys Glu Leu Gly Gly Ala Phe
 35 40

<210> 44

<211> 41

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: CALGRANULIN B

<400> 44

Glu Ser Ser Ile Glu Thr Ile Ile Asn Ile Phe His Gln Tyr Ser Val
 1 5 10 15

Arg Leu Gly His Tyr Asp Thr Leu Ile Gln Lys Glu Phe Lys Gln Leu
 20 25 30

Val Gln Lys Glu Leu Pro Asn Phe Leu
 35 40

<210> 45

<211> 10

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Consensus sequence

<400> 45
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<210> 46
<211> 41
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: CALGRANULIN B

<400> 46
Glu Arg Ser Ile Thr Thr Ile Ile Asp Thr Phe His Gln Tyr Ser Arg
1 5 10 15

Lys Glu Gly His Pro Asp Thr Leu Ser Lys Lys Glu Phe Arg Gln Met
20 25 30

Val Glu Ala Gln Leu Ala Thr Phe Met
35 40

<210> 47
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Consensus
sequence

<400> 47
Glu Ile Phe His Gln Tyr Ser Gly Leu Glu Leu
1 5 10

<210> 48
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Unknown Organism: reverse strand sequence of SEQ ID
NO:4 (GenBank AA315020)

<220>
<221> misc_feature
<222> (21)..(21)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (127)..(127)
<223> n is a, c, g, or t

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